



SEQUENCE LISTING

<110> Salkoff, Lawrence
Schreiber, Matthew
Silvia, Chris
The Washington University
ICAgene Inc.

<120> A pH Sensitive Potassium Channel in Spermatocytes

<130> 018512-000120US

<140> 09/176,664

<141> 1998-10-21

<150> US 60/063,138

<151> 1997-10-22

<150> US 60/076,172

<151> 1998-02-27

<160> 53

<170> PatentIn Ver. 2.0

<210> 1

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<212> PRT

<213> Mus musculus

<220>

<223> mouse Slo3 (mSlo3)

<220>

<221> VARIANT

<222> (5)

<223> polymorphic variant #2 Leu -> Ile

<220>

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<222> (21)

<223> polymorphic variant #1 Ile -> Val

<220>

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<222> (25)

<223> polymorphic variant #3 Ala -> Ser

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Ala Thr Phe Phe Gly Gly Leu Ile Ile Leu Phe Leu Phe Arg Ile Ala
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 Leu Tyr Phe His Gly Val Phe Arg Gln Arg Ile Glu Met Leu Leu Ser
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 Ala Gln Thr Val Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
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 Ser Ile Gly Ser Leu Val Ile Tyr Phe Ile Asn Ser Met Asp Pro Val
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 Arg Arg Cys Ser Ser Tyr Glu Asp Lys Ile Val His Gly Asp Leu Ser
 130 135 140
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Trp Ala Ala
 145 150 155 160
 Glu Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
 165 170 175
 Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp
 180 185 190
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Lys
 195 200 205
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 Ser Lys Leu Leu Ser Ile Val Ile Ser Thr Trp Phe Thr Ala Ala Gly
 225 230 235 240
 Phe Leu His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Asn Gly Arg
 245 250 255
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 260 265 270
 Thr Met Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
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 Gly Arg Ile Phe Ile Val Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
 290 295 300
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ser Thr Arg Lys Lys
 305 310 315 320
 Tyr Thr Lys Pro Tyr Glu Ala Val Lys Gly Lys Lys Phe Ile Val Val
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 405 410 415
 His Phe Cys Ser Asp Leu His Asp Glu Asp Asn Ser Asn Ile Met Arg
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 Trp Gln Lys His Phe Leu Asn Gly Leu Lys Asn Lys Ile Leu Thr Gln
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 Pro Phe Phe His Ser Cys Cys Thr Leu Ile Leu Asn Pro Ser Ser Gln
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 Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile
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Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys
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Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe
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Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile
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<212> DNA

<213> Mus musculus

<220>

<223> mouse Slo3 (mSlo3)

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atcttattcc	ttttcagaat	agccttgaaa	agctcaagaa	gttggaata	cgtcaagggg	180
ccaagaggac	tcttggaact	attctcatca	cgtagaatcg	aggctaattc	tttgaggaaa	240
ctttactttc	atggagtatt	tcgtcagcgc	atcgaaatgc	tgctttctgc	acagaccgtc	300
gtggggcaag	tggttggtgat	ccttgtcttt	gtactaagca	tcgggtctct	tgtgatctat	360
ttcatcaatt	caatggatcc	tggtcgaagg	tggtcttcat	atgaagacaa	aattgtccat	420
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aaaatcaaga	gccgacaaca	actcatagca	ccgaccatca	tggtgatgaa	aagcagcttg	1920
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<210> 3
<211> 112
<212> PRT
<213> Homo sapiens

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<223> human Slo3-a (hSlo3-a)

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<222> (29)
<223> Xaa = any amino acid

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Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
 35             40             45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
 50             55             60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
 65             70             75             80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
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 <213> Homo sapiens

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 ttccagggac aatttcgtga tcatatagaa atgttgcttt cagcccagac ctttgtgggg 240
 caagtgttgg tgatccttgt ctttgtacta agcattgggt ctcttataat ctatttcato 300
 aattcwgctg accctgttgg aacgctgttc atcatatgaa gacaaaacca ttcctattga 360
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<210> 6
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 <212> PRT
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 Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
 35 40 45
 Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
 50 55 60
 Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
 65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
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Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val Gly Thr Leu Phe Ile Ile
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<213> Homo sapiens

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<222> (29)
<223> Xaa = any amino acid

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Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
35 40 45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
50 55 60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
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Ile Tyr Phe Ile Asn Ser Met Asp Pro Val Gly Thr Leu Phe Ile Ile
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<210> 8
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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26

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<213> Artificial Sequence

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<220>
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<210> 14
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<220>
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<210> 15
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<212> DNA
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24

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<212> PRT
<213> Homo sapiens

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<220>
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<222> (25)
<223> polymorphic variant #3 Ala -> Ser

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35 40 45
Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile
50 55 60
Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser
65 70 75 80
Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser
85 90 95

Ala Gln Thr Phe Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
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 Ser Ile Gly Ser Leu Ile Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val
 115 120 125
 Gly Ser Cys Ser Ser Tyr Glu Asp Lys Thr Ile Pro Ile Asp Leu Val
 130 135 140
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Met Ala Ala
 145 150 155 160
 Asp Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
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 Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp
 180 185 190
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Gln
 195 200 205
 Ile Leu Gln Ile Leu Arg Ala Ile Lys Thr Ser Asn Ser Val Lys Phe
 210 215 220
 Ser Lys Leu Leu Ser Ile Ile Leu Ser Thr Trp Phe Thr Ala Ala Gly
 225 230 235 240
 Phe Ile His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Lys Gly Arg
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 Asn Ser Gln Asn Ile Ser Tyr Phe Glu Ser Ile Tyr Leu Val Met Ala
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 Thr Thr Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
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 Gly Arg Thr Phe Ile Met Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
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 Ala Tyr Thr Thr Phe Ile Ser Gly Ser Ala Met Lys Trp Glu Asp Leu
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 Arg Arg Val Ala Val Glu Ser Ala Glu Ala Cys Leu Ile Ile Ala Asn
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Pro Leu Cys Ser Asp Ser His Ala Glu Asp Ile Ser Asn Ile Met Arg
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 Val Leu Ser Ile Lys Asn Tyr Asp Ser Thr Thr Arg Ile Ile Ile Gln
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 Ile Leu Gln Ser His Asn Lys Val Tyr Leu Pro Lys Ile Pro Ser Trp
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 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu
 485 490 495
 Thr Ser Leu Phe Val Glu Gln Asn Lys Lys Val Met Pro Lys Gln Thr
 500 505 510
 Trp Lys Lys His Phe Leu Asn Ser Met Lys Asn Lys Ile Leu Thr Gln
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 Arg Leu Ser Asp Asp Phe Ala Gly Met Ser Phe Pro Glu Val Ala Arg
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 545 550 555 560
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 580 585 590
 Pro Lys Asp Val Arg Arg Ala Leu Phe Tyr Cys Ser Val Cys His Asp
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 Ser Arg Gln His Ile Thr Val Pro Ser Val Lys Arg Met Lys Lys Cys
 625 630 635 640
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 Phe His Trp Cys Lys Pro Thr Ser Leu Asp Lys Val Thr Leu Lys Arg
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 Thr Gly Lys Ser Lys Tyr Lys Phe Arg Asn His Ile Val Ala Cys Val
 705 710 715 720
 Phe Gly Asp Ala His Ser Ala Pro Met Gly Leu Arg Asn Phe Val Met
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Pro Leu Arg Ala Ser Asn Tyr Thr Arg Lys Glu Leu Lys Asp Ile Val
 740 745 750
 Phe Ile Gly Ser Leu Asp Tyr Leu Gln Arg Glu Trp Arg Phe Leu Arg
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 770 775 780
 Asp Leu His Ala Ala Asn Ile Glu Gln Cys Ser Met Cys Ala Val Leu
 785 790 795 800
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<213> Homo sapiens

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<223> human hSlo3-2 (hSlo3-2)

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Ala	Asn	Tyr	Ile	Pro	Glu	Met	Val	Glu	Leu	Phe	Ser	Thr	Arg	Lys	Lys	305	310	315
Tyr	Thr	Lys	Pro	Tyr	Glu	Ala	Val	Lys	Gly	Lys	Lys	Phe	Ile	Val	Val	325	330	335
Cys	Gly	Asn	Ile	Thr	Val	Asp	Ser	Val	Thr	Ala	Phe	Leu	Arg	Asn	Phe	340	345	350
Leu	His	Trp	Lys	Ser	Gly	Glu	Ile	Asn	Ile	Glu	Ile	Val	Phe	Leu	Gly	355	360	365
Glu	Thr	Leu	Pro	Cys	Leu	Glu	Leu	Glu	Thr	Leu	Leu	Lys	Cys	His	Thr	370	375	380
Ser	Cys	Thr	Asn	Phe	Val	Cys	Gly	Thr	Ala	Leu	Lys	Phe	Glu	Asp	Leu	385	390	395
Lys	Arg	Val	Ala	Val	Glu	Asn	Ser	Glu	Ala	Cys	Leu	Ile	Leu	Ala	Asn	405	410	415
His	Phe	Cys	Ser	Asp	Leu	His	Asp	Glu	Asp	Asn	Ser	Asn	Ile	Met	Arg	420	425	430
Val	Leu	Ser	Ile	Lys	Asn	Tyr	Tyr	Pro	Gln	Thr	Arg	Val	Ile	Ile	Gln	435	440	445
Ile	Leu	Gln	Ser	Gln	Asn	Lys	Val	Phe	Leu	Ser	Lys	Ile	Pro	Asn	Trp	450	455	460
Asp	Trp	Ser	Ala	Gly	Asp	Asn	Ile	Leu	Cys	Phe	Ala	Glu	Leu	Lys	Leu	465	470	475
Gly	Phe	Ile	Ala	Gln	Gly	Cys	Leu	Val	Pro	Gly	Leu	Cys	Thr	Phe	Leu	485	490	495
Thr	Thr	Leu	Phe	Ile	Glu	Gln	Asn	Gln	Lys	Val	Phe	Pro	Lys	His	Pro	500	505	510
Trp	Gln	Lys	His	Phe	Leu	Asn	Gly	Leu	Lys	Asn	Lys	Ile	Leu	Thr	Gln	515	520	525
Arg	Leu	Ser	Asn	Asp	Phe	Val	Gly	Met	Thr	Phe	Pro	Gln	Val	Ser	Arg	530	535	540
Leu	Cys	Phe	Val	Lys	Leu	Asn	Leu	Met	Leu	Ile	Ala	Ile	Gln	His	Lys	545	550	555
Pro	Phe	Phe	His	Ser	Cys	Cys	Thr	Leu	Ile	Leu	Asn	Pro	Ser	Ser	Gln	565	570	575
Val	Arg	Leu	Asn	Lys	Asp	Thr	Leu	Gly	Phe	Phe	Ile	Ala	Asp	Ser	Ser	580	585	590

Lys Ala Val Lys Arg Ala Phe Phe Tyr Cys Ser Asn Cys His Ser Asp
 595 600 605
 Val Cys Asn Pro Glu Leu Ile Gly Lys Cys Asn Cys Lys Ile Lys Ser
 610 615 620
 Arg Gln Gln Leu Ile Ala Pro Thr Ile Met Val Met Lys Ser Ser Leu
 625 630 635 640
 Thr Asp Phe Thr Thr Ser Ser His Ile His Ala Ser Met Ser Thr Glu
 645 650 655
 Ile His Thr Cys Phe Ser Arg Glu Gln Pro Ser Leu Ile Thr Ile Thr
 660 665 670
 Thr Asn Arg Pro Thr Thr Asn Asp Thr Val Asp Asp Thr Asp Met Leu
 675 680 685
 Asp Ser Ser Gly Met Phe His Trp Cys Arg Ala Met Pro Leu Asp Lys
 690 695 700
 Val Val Leu Lys Arg Ser Glu Lys Ala Lys His Glu Phe Gln Asn His
 705 710 715 720
 Ile Val Val Cys Val Phe Gly Asp Ala Gln Cys Thr Leu Val Gly Leu
 725 730 735
 Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr Arg Gln Glu
 740 745 750
 Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Glu Tyr Phe Gln Arg Glu
 755 760 765
 Trp Arg Phe Leu Arg Asn Phe Pro Lys Ile His Ile Met Pro Gly Ser
 770 775 780
 Ala Leu Tyr Met Gly Asp Leu Ile Ala Val Asn Val Glu Gln Cys Ser
 785 790 795 800
 Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile
 805 810 815
 Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Asn Ile Gln Ser Leu
 820 825 830
 Arg Ile Thr Ser Pro Thr Pro Gly Ser Ser Lys Ser Glu Val Lys Pro
 835 840 845
 Ser Ser Ala Phe Asp Ser Lys Glu Arg Lys Gln Arg Tyr Lys Gln Ile
 850 855 860
 Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu
 865 870 875 880
 Gln Met Gly Gly Leu Asp Gly Met Leu Lys Gly Thr Ser Leu His Leu
 885 890 895
 Ser Thr Ser Phe Ser Thr Gly Ala Val Phe Ser Asp Thr Phe Leu Asp
 900 905 910

Ser Leu Leu Ala Thr Ser Phe Tyr Asn Tyr His Val Val Glu Leu Leu
 915 920 925
 Gln Met Leu Val Thr Gly Gly Ile Ser Ser Glu Met Glu His Tyr Leu
 930 935 940
 Val Lys Glu Lys Pro Tyr Lys Thr Thr Asp Asp Tyr Glu Ala Ile Lys
 945 950 955 960
 Ser Gly Arg Thr Arg Cys Lys Leu Gly Leu Leu Ser Leu Asp Gln Thr
 965 970 975
 Val Leu Ser Gly Ile Asn Pro Arg Lys Thr Phe Gly Gln Leu Phe Cys
 980 985 990
 Gly Ser Leu Asp Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met
 995 1000 1005
 Ile Asp Glu Glu Glu Pro Ser Gln Glu His Lys Arg Phe Val Ile Thr
 1010 1015 1020
 Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys
 1025 1030 1035 1040
 Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe
 1045 1050 1055
 Asn Phe Arg Leu Lys Thr Thr Leu Gln Thr Arg Arg Arg His Trp Pro
 1060 1065 1070
 Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile
 1075 1080 1085
 Phe Thr Gln Ser Thr Thr Arg Glu Arg Gly Gly Leu Ser Thr Thr Thr
 1090 1095 1100
 Pro Glu Ser Ile Leu Trp Thr Arg Gln Leu Phe Cys Gly Ser Leu Asp
 1105 1110 1115 1120
 Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met Ile Asp
 1125 1130

<210> 21
 <211> 1236
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse Slo1 (mSlo1)

<400> 21
 Met Asp Ala Leu Ile Ile Pro Val Thr Met Glu Val Pro Cys Asp Ser
 1 5 10 15
 Arg Gly Gln Arg Met Trp Trp Ala Phe Leu Ala Ser Ser Met Val Thr
 20 25 30
 Phe Phe Gly Gly Leu Phe Ile Ile Leu Leu Trp Arg Thr Leu Lys Tyr
 35 40 45

Leu Trp Thr Val Cys Cys His Cys Gly Gly Lys Thr Lys Glu Ala Gln
 50 55 60
 Lys Ile Asn Asn Gly Ser Ser Gln Ala Asp Gly Thr Leu Lys Pro Val
 65 70 75 80
 Asp Glu Lys Glu Glu Val Val Ala Ala Glu Val Gly Trp Met Thr Ser
 85 90 95
 Val Lys Asp Trp Ala Gly Val Met Ile Ser Ala Gln Thr Leu Thr Gly
 100 105 110
 Arg Val Leu Val Val Leu Val Phe Ala Leu Ser Ile Gly Ala Leu Val
 115 120 125
 Ile Tyr Phe Ile Asp Ser Ser Asn Pro Ile Glu Ser Cys Gln Asn Phe
 130 135 140
 Tyr Lys Asp Phe Thr Leu Gln Ile Asp Met Ala Phe Asn Val Phe Phe
 145 150 155 160
 Leu Leu Tyr Phe Gly Leu Arg Phe Ile Ala Ala Asn Asp Lys Leu Trp
 165 170 175
 Phe Trp Leu Glu Val Asn Ser Val Val Asp Phe Phe Thr Val Pro Pro
 180 185 190
 Val Phe Val Ser Val Tyr Leu Asn Arg Ser Trp Leu Gly Leu Arg Phe
 195 200 205
 Leu Arg Ala Leu Arg Leu Ile Gln Phe Ser Glu Ile Leu Gln Phe Leu
 210 215 220
 Asn Ile Leu Lys Thr Ser Asn Ser Ile Lys Leu Val Asn Leu Leu Ser
 225 230 235 240
 Ile Phe Ile Ser Thr Trp Leu Thr Ala Ala Gly Phe Ile His Leu Val
 245 250 255
 Glu Asn Ser Gly Asp Pro Trp Glu Asn Phe Gln Asn Asn Gln Ala Leu
 260 265 270
 Thr Tyr Trp Glu Cys Val Tyr Leu Leu Met Val Thr Met Ser Thr Val
 275 280 285
 Gly Tyr Gly Asp Val Tyr Ala Lys Thr Thr Leu Gly Arg Leu Phe Met
 290 295 300
 Val Phe Phe Ile Leu Gly Gly Leu Ala Met Phe Ala Ser Tyr Val Pro
 305 310 315 320
 Glu Ile Ile Glu Leu Ile Gly Asn Arg Lys Lys Tyr Gly Gly Ser Tyr
 325 330 335
 Ser Ala Val Ser Gly Arg Lys His Ile Val Val Cys Gly His Ile Thr
 340 345 350
 Leu Glu Ser Val Ser Asn Phe Leu Lys Asp Phe Leu His Lys Asp Arg
 355 360 365

Asp	Asp	Val	Asn	Val	Glu	Ile	Val	Phe	Leu	His	Asn	Ile	Ser	Pro	Asn	370	375	380
Leu	Glu	Leu	Glu	Ala	Leu	Phe	Lys	Arg	His	Phe	Thr	Gln	Val	Glu	Phe	385	390	395
Tyr	Gln	Gly	Ser	Val	Leu	Asn	Pro	His	Asp	Leu	Ala	Arg	Val	Lys	Ile	405	410	415
Glu	Ser	Ala	Asp	Ala	Cys	Leu	Ile	Leu	Ala	Asn	Lys	Tyr	Cys	Ala	Asp	420	425	430
Pro	Asp	Ala	Glu	Asp	Ala	Ser	Asn	Ile	Met	Arg	Val	Ile	Ser	Ile	Lys	435	440	445
Asn	Tyr	His	Pro	Lys	Ile	Arg	Ile	Ile	Thr	Gln	Met	Leu	Gln	Tyr	His	450	455	460
Asn	Lys	Ala	His	Leu	Leu	Asn	Ile	Pro	Ser	Trp	Asn	Trp	Lys	Glu	Gly	465	470	475
Asp	Asp	Ala	Ile	Cys	Leu	Ala	Glu	Leu	Lys	Leu	Gly	Phe	Ile	Ala	Gln	485	490	495
Ser	Cys	Leu	Ala	Gln	Gly	Leu	Ser	Thr	Met	Leu	Ala	Asn	Leu	Phe	Ser	500	505	510
Met	Arg	Ser	Phe	Ile	Lys	Ile	Glu	Glu	Asp	Thr	Trp	Gln	Lys	Tyr	Tyr	515	520	525
Leu	Glu	Gly	Val	Ser	Asn	Glu	Met	Tyr	Thr	Glu	Tyr	Leu	Ser	Ser	Ala	530	535	540
Phe	Val	Gly	Leu	Ser	Phe	Pro	Thr	Val	Cys	Glu	Leu	Cys	Phe	Val	Lys	545	550	555
Leu	Lys	Leu	Leu	Met	Ile	Ala	Ile	Glu	Tyr	Lys	Ser	Ala	Asn	Arg	Glu	565	570	575
Ser	Arg	Ile	Leu	Ile	Asn	Pro	Gly	Asn	His	Leu	Lys	Ile	Gln	Glu	Gly	580	585	590
Thr	Leu	Gly	Phe	Phe	Ile	Ala	Ser	Asp	Ala	Lys	Glu	Val	Lys	Arg	Ala	595	600	605
Phe	Phe	Tyr	Cys	Lys	Ala	Cys	His	Asp	Asp	Val	Thr	Asp	Pro	Lys	Arg	610	615	620
Ile	Lys	Lys	Cys	Gly	Cys	Arg	Arg	Leu	Ile	Tyr	Phe	Glu	Asp	Glu	Gln	625	630	635
Pro	Pro	Thr	Leu	Ser	Pro	Lys	Lys	Lys	Gln	Arg	Asn	Gly	Gly	Met	Arg	645	650	655
Asn	Ser	Pro	Asn	Thr	Ser	Pro	Lys	Leu	Met	Arg	His	Asp	Pro	Leu	Leu	660	665	670
Ile	Pro	Gly	Asn	Asp	Gln	Ile	Asp	Asn	Met	Asp	Ser	Asn	Val	Lys	Lys	675	680	685

Tyr Asp Ser Thr Gly Met Phe His Trp Cys Ala Pro Lys Glu Ile Glu
 690 695 700
 Lys Val Ile Leu Thr Arg Ser Glu Ala Ala Met Thr Val Leu Ser Gly
 705 710 715 720
 His Val Val Val Cys Ile Phe Gly Asp Val Ser Ser Ala Leu Ile Gly
 725 730 735
 Leu Arg Asn Leu Val Met Pro Leu Arg Ala Ser Asn Phe His Tyr His
 740 745 750
 Glu Leu Lys His Ile Val Phe Val Gly Ser Ile Glu Tyr Leu Lys Arg
 755 760 765
 Glu Trp Glu Thr Leu His Asn Phe Pro Lys Val Ser Ile Leu Pro Gly
 770 775 780
 Thr Pro Leu Ser Arg Ala Asp Leu Arg Ala Val Asn Ile Asn Leu Cys
 785 790 795 800
 Asp Met Cys Val Ile Leu Ser Ala Asn Gln Asn Asn Ile Asp Asp Thr
 805 810 815
 Ser Leu Gln Asp Lys Glu Cys Ile Leu Ala Ser Leu Asn Ile Lys Ser
 820 825 830
 Met Gln Phe Asp Asp Ser Ile Gly Val Leu Gln Ala Asn Ser Gln Gly
 835 840 845
 Phe Thr Pro Pro Gly Met Asp Arg Ser Ser Pro Asp Asn Ser Pro Val
 850 855 860
 His Gly Met Leu Arg Gln Pro Ser Ile Thr Thr Gly Val Asn Ile Pro
 865 870 875 880
 Ile Ile Thr Glu Leu Val Asn Asp Thr Asn Val Gln Phe Leu Asp Gln
 885 890 895
 Asp Asp Asp Asp Asp Pro Asp Thr Glu Leu Tyr Leu Thr Gln Pro Phe
 900 905 910
 Ala Cys Gly Thr Ala Phe Ala Val Ser Val Leu Asp Ser Leu Met Ser
 915 920 925
 Ala Thr Tyr Phe Asn Asp Asn Ile Leu Thr Leu Ile Arg Thr Leu Val
 930 935 940
 Thr Gly Gly Ala Thr Pro Glu Leu Glu Ala Leu Ile Ala Glu Glu Asn
 945 950 955 960
 Ala Leu Arg Gly Gly Tyr Ser Thr Pro Gln Thr Leu Ala Asn Arg Asp
 965 970 975
 Arg Cys Arg Val Ala Gln Leu Ala Leu Leu Asp Gly Pro Phe Ala Asp
 980 985 990
 Leu Gly Asp Gly Gly Cys Tyr Gly Asp Leu Phe Cys Lys Ala Leu Lys
 995 1000 1005

Thr Tyr Asn Met Leu Cys Phe Gly Ile Tyr Arg Leu Arg Asp Ala His
 1010 1015 1020
 Leu Ser Thr Pro Ser Gln Cys Thr Lys Arg Tyr Val Ile Thr Asn Pro
 1025 1030 1035 1040
 Pro Tyr Glu Phe Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met
 1045 1050 1055
 Gln Phe Asp His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser
 1060 1065 1070
 Ser His Ser Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser
 1075 1080 1085
 Ile Pro Ser Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser
 1090 1095 1100
 Arg Asp Lys Gln Asn Ala Thr Arg Met Thr Arg Met Gly Gln Ala Glu
 1105 1110 1115 1120
 Lys Lys Trp Phe Thr Asp Glu Pro Asp Asn Ala Tyr Pro Arg Asn Ile
 1125 1130 1135
 Gln Ile Lys Pro Met Ser Thr His Met Ala Asn Gln Ile Asn Gln Tyr
 1140 1145 1150
 Lys Ser Thr Ser Ser Leu Ile Pro Pro Ile Arg Glu Val Glu Asp Glu
 1155 1160 1165
 Cys Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met Gln Phe Asp
 1170 1175 1180
 His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser Ser His Ser
 1185 1190 1195 1200
 Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser Ile Pro Ser
 1205 1210 1215
 Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser Arg Asp Lys
 1220 1225 1230
 Gln Asn Ala Thr
 1235

<210> 22
 <211> 1262
 <212> PRT
 <213> Drosophila sp.

<220>
 <223> Drosophila Slol (dSlol)

<400> 22
 Met Ala Ser Gly Leu Ile Asp Thr Asn Phe Ser Ser Thr Leu Ala Asn
 1 5 10 15
 Gly Met Ser Gly Cys Asp Gln Ser Thr Val Glu Pro Leu Ala Asp Asp
 20 25 30

Pro Thr Asp Ser Pro Phe Asp Ala Asp Asp Cys Leu Lys Val Arg Lys
 35 40 45
 Tyr Trp Cys Phe Leu Leu Ser Ser Ile Phe Thr Phe Leu Ala Gly Leu
 50 55 60
 Leu Val Val Leu Leu Trp Arg Ala Phe Ala Phe Val Ser Cys Arg Lys
 65 70 75 80
 Glu Pro Asp Leu Gly Pro Asn Asp Pro Lys Gln Lys Glu Gln Lys Ala
 85 90 95
 Ser Arg Asn Lys Gln Glu Phe Glu Gly Thr Phe Met Thr Glu Ala Lys
 100 105 110
 Asp Trp Ala Gly Glu Leu Ile Ser Gly Gln Thr Thr Thr Gly Arg Ile
 115 120 125
 Leu Val Val Leu Val Phe Ile Leu Ser Ile Ala Ser Leu Ile Ile Tyr
 130 135 140
 Phe Val Asp Ala Ser Ser Glu Glu Val Glu Arg Cys Gln Lys Trp Ser
 145 150 155 160
 Asn Asn Ile Thr Gln Gln Ile Asp Leu Ala Phe Asn Ile Phe Phe Met
 165 170 175
 Val Tyr Phe Phe Ile Arg Phe Ile Ala Ala Ser Asp Lys Leu Trp Phe
 180 185 190
 Met Leu Glu Met Tyr Ser Phe Val Asp Tyr Phe Thr Ile Pro Pro Ser
 195 200 205
 Phe Val Ser Ile Tyr Leu Asp Arg Thr Trp Ile Gly Leu Arg Phe Leu
 210 215 220
 Arg Ala Leu Arg Leu Met Thr Val Pro Asp Ile Leu Gln Tyr Leu Asn
 225 230 235 240
 Val Leu Lys Thr Ser Ser Ser Ile Arg Leu Ala Gln Leu Val Ser Ile
 245 250 255
 Phe Ile Ser Val Trp Leu Thr Ala Ala Gly Ile Ile His Leu Leu Glu
 260 265 270
 Asn Ser Gly Asp Pro Leu Asp Phe Asn Asn Ala His Arg Leu Ser Tyr
 275 280 285
 Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly Tyr
 290 295 300
 Gly Asp Val Tyr Cys Glu Thr Val Leu Gly Arg Thr Phe Leu Val Phe
 305 310 315 320
 Phe Leu Leu Val Gly Leu Ala Val Phe Ala Ser Trp Ile Pro Glu Ile
 325 330 335
 Thr Glu Leu Ala Ala Gln Arg Ser Lys Tyr Gly Gly Thr Tyr Ser Lys
 340 345 350

Asp	Pro	Arg	Lys	Arg	His	Ile	Val	Val	Cys	Gly	His	Ile	Thr	Tyr	Glu	355	360	365	
Ser	Val	Ser	His	Phe	Leu	Lys	Asp	Phe	Leu	His	Glu	Asp	Arg	Glu	Asp	370	375	380	
Val	Asp	Val	Glu	Val	Val	Phe	Leu	His	Arg	Lys	Pro	Pro	Asp	Leu	Glu	385	390	395	400
Leu	Glu	Gly	Leu	Phe	Lys	Arg	His	Phe	Thr	Thr	Val	Glu	Phe	Phe	Gln	405	410	415	
Gly	Thr	Ile	Met	Asn	Pro	Ile	Asp	Leu	Gln	Arg	Val	Lys	Val	His	Glu	420	425	430	
Ala	Asp	Ala	Cys	Leu	Val	Leu	Ala	Asn	Lys	Tyr	Cys	Gln	Asp	Pro	Asp	435	440	445	
Ala	Glu	Asp	Ala	Ala	Asn	Ile	Met	Arg	Val	Ile	Ser	Ile	Lys	Asn	Tyr	450	455	460	
Ser	Asp	Asp	Ile	Arg	Val	Ile	Ile	Gln	Leu	Met	Gln	Tyr	His	Asn	Lys	465	470	475	480
Ala	Tyr	Leu	Leu	Asn	Ile	Pro	Ser	Trp	Asp	Trp	Lys	Gln	Gly	Asp	Asp	485	490	495	
Val	Ile	Cys	Leu	Ala	Glu	Leu	Lys	Leu	Gly	Phe	Ile	Ala	Gln	Ser	Cys	500	505	510	
Leu	Ala	Pro	Gly	Phe	Ser	Thr	Met	Met	Ala	Asn	Leu	Phe	Ala	Met	Arg	515	520	525	
Ser	Phe	Lys	Thr	Ser	Pro	Asp	Met	Gln	Ser	Trp	Thr	Asn	Asp	Tyr	Leu	530	535	540	
Arg	Gly	Thr	Gly	Met	Glu	Met	Tyr	Thr	Glu	Thr	Leu	Ser	Pro	Thr	Phe	545	550	555	560
Ile	Gly	Ile	Pro	Phe	Ala	Gln	Ala	Thr	Glu	Leu	Cys	Phe	Ser	Lys	Leu	565	570	575	
Lys	Leu	Leu	Leu	Leu	Ala	Ile	Glu	Ile	Lys	Gly	Ala	Glu	Glu	Gly	Ala	580	585	590	
Asp	Ser	Lys	Ile	Ser	Ile	Asn	Pro	Arg	Gly	Ala	Lys	Ile	Gln	Ala	Asn	595	600	605	
Thr	Gln	Gly	Phe	Phe	Ile	Ala	Gln	Ser	Ala	Asp	Glu	Val	Lys	Arg	Ala	610	615	620	
Trp	Phe	Tyr	Cys	Lys	Ala	Cys	His	Glu	Asp	Ile	Lys	Asp	Glu	Thr	Leu	625	630	635	640
Ile	Lys	Lys	Cys	Lys	Cys	Lys	Asn	Leu	Thr	Val	Gln	Pro	Arg	Ser	Lys	645	650	655	
Phe	Asp	Asp	Leu	Gly	Asp	Ile	Thr	Arg	Asp	Arg	Glu	Asp	Thr	Asn	Leu	660	665	670	

Leu Asn Arg Asn Val Arg Arg Pro Asn Gly Thr Gly Asn Gly Thr Gly
 675 680 685
 Gly Met His His Met Asn Ser Thr Arg Ala Ala Ala Ala Ala Ala
 690 695 700
 Ala Ala Gly Lys Gln Val Asn Lys Val Lys Pro Thr Val Asn Val Ser
 705 710 715 720
 Arg Gln Val Glu Gly Gln Val Ile Ser Pro Ser Gln Tyr Asn Arg Pro
 725 730 735
 Thr Ser Arg Ser Ser Gly Thr Gly Thr Gln Asn Gln Asn Gly Gly Val
 740 745 750
 Ser Leu Pro Ala Gly Ile Ala Asp Asp Gln Ser Lys Asp Phe Asp Phe
 755 760 765
 Glu Lys Thr Glu Met Lys Tyr Asp Ser Thr Gly Met Phe His Trp Ser
 770 775 780
 Pro Ala Lys Ser Leu Gln Asp Cys Ile Leu Asp Arg Asn Gln Ala Ala
 785 790 795 800
 Met Thr Val Leu Asn Gly His Val Val Val Cys Leu Phe Ala Asp Pro
 805 810 815
 Asp Ser Pro Leu Ile Gly Leu Arg Asn Leu Val Met Pro Leu Arg Ala
 820 825 830
 Ser Asn Phe His Tyr His Glu Leu Lys His Val Val Ile Val Gly Ser
 835 840 845
 Val Asp Tyr Ile Arg Arg Glu Trp Lys Met Leu Gln Asn Leu Pro Lys
 850 855 860
 Ile Ser Val Leu Asn Gly Ser Pro Leu Ser Arg Ala Asp Leu Arg Ala
 865 870 875 880
 Val Asn Val Asn Leu Cys Asp Met Cys Cys Ile Leu Ser Ala Lys Val
 885 890 895
 Pro Ser Asn Asp Asp Pro Thr Leu Ala Asp Lys Glu Ala Ile Leu Ala
 900 905 910
 Ser Leu Asn Ile Lys Ala Met Thr Phe Asp Asp Thr Ile Gly Val Leu
 915 920 925
 Ser Gln Arg Gly Pro Glu Phe Asp Asn Leu Ser Ala Thr Ala Gly Ser
 930 935 940
 Pro Ile Val Leu Gln Arg Arg Gly Ser Val Tyr Gly Ala Asn Val Pro
 945 950 955 960
 Met Ile Thr Glu Leu Val Asn Asp Gly Asn Val Gln Phe Leu Asp Gln
 965 970 975
 Asp Asp Asp Asp Asp Pro Asp Thr Glu Leu Tyr Leu Thr Gln Pro Phe
 980 985 990

Ala Cys Gly Thr Ala Phe Ala Val Ser Val Leu Asp Ser Leu Met Ser
 995 1000 1005
 Thr Thr Tyr Phe Asn Gln Asn Ala Leu Thr Leu Ile Arg Ser Leu Ile
 1010 1015 1020
 Thr Gly Gly Ala Thr Pro Glu Leu Glu Leu Ile Leu Ala Glu Gly Ala
 1025 1030 1035 1040
 Gly Leu Arg Gly Gly Tyr Ser Thr Val Glu Ser Leu Ser Asn Arg Asp
 1045 1050 1055
 Arg Cys Arg Val Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln
 1060 1065 1070
 Phe Gly Glu Cys Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys
 1075 1080 1085
 Ser Tyr Gly Met Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser
 1090 1095 1100
 Ser Ser Cys Asp Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro
 1105 1110 1115 1120
 Asp Asp Phe Ser Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln
 1125 1130 1135
 Phe Asp Pro Gly Leu Glu Tyr Lys Pro Pro Ala Val Arg Ala Pro Ala
 1140 1145 1150
 Gly Gly Arg Gly Thr Asn Thr Gln Gly Ser Gly Val Gly Gly Gly Gly
 1155 1160 1165
 Ser Asn Lys Asp Asp Asn Ser Leu Ser Asn Arg Asp Arg Cys Arg Val
 1170 1175 1180
 Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln Phe Gly Glu Cys
 1185 1190 1195 1200
 Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys Ser Tyr Gly Met
 1205 1210 1215
 Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser Ser Ser Cys Asp
 1220 1225 1230
 Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro Asp Asp Phe Ser
 1235 1240 1245
 Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln Phe Asp
 1250 1255 1260

<210> 23

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:sense
 oligonucleotide

<400> 23
 gtggatgata ccgacatgct ggac 24

<210> 24
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:antisense
 oligonucleotide

<400> 24
 gagaccacct ctctcccgtg tcgt 24

<210> 25
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mSlo3 (S4 to
 S5) sense primer

<400> 25
 ctcgaactcc ctaaaatctt acagat 26

<210> 26
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mSlo3 (S4 to
 S5) antisense primer

<400> 26
 ttccgttgag ccaggggtca ccagaatt 28

<210> 27
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mSlo3 (S8 to
 S9) sense primer

<400> 27
 tctgctttgt gaagctaaat ct 22

<210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mSlo3 (S8 to S9) antisense primer

 <400> 28
 tttcaaagcc tcttttagcgg taa 23

 <210> 29
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:mSlo3 (S9 to S10) sense primer

 <400> 29
 ttatgcctgg atctgcactc tacatg 26

 <210> 30
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:mSlo3 (S9 to S10) antisense primer

 <400> 30
 atagtttccg tctactaccg aaa 23

 <210> 31
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:control human beta-actin sense primer

 <400> 31
 gatgatatcg ccgcgctcgt cgtcgac 27

 <210> 32
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:control human beta-actin antisense primer

 <400> 32
 tcggtccagg tctgcgtcct accgtac 27

<210> 33
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
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 sense primer

 <400> 33
 cggaacgctc atgtacaatc gaaatcca 28

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 antisense primer

 <400> 34
 ttccgttgag ccaggggtca ccagaatt 28

 <210> 35
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 <220>
 <223> Description of Artificial Sequence:human testis
 cDNA library primer

 <400> 35
 ggcagcgctc attctttcct cctt 24

 <210> 36
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 <223> Description of Artificial Sequence:human testis
 cDNA library primer

 <400> 36
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 <210> 37
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<400> 37
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<210> 38
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<210> 39
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<400> 39
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<210> 41
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<210> 42
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<210> 43
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<210> 44
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Gly Thr Ala Phe
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<210> 45
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and mSlo3 sequences at C-terminal end of chimera
Region B fragment

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<210> 46
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<400> 46
Ser Thr Ser Phe
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<210> 47
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<210> 48
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<400> 48
Thr Gln Pro Phe
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<210> 49
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<400> 49
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<210> 50
<211> 4
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<210> 51
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His Leu Leu Pro
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<210> 52
<211> 4
<212> PRT
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Glu Leu Glu Ala
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<210> 53
<211> 4
<212> PRT
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a/ <400> 53
Glu Leu Val Pro
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